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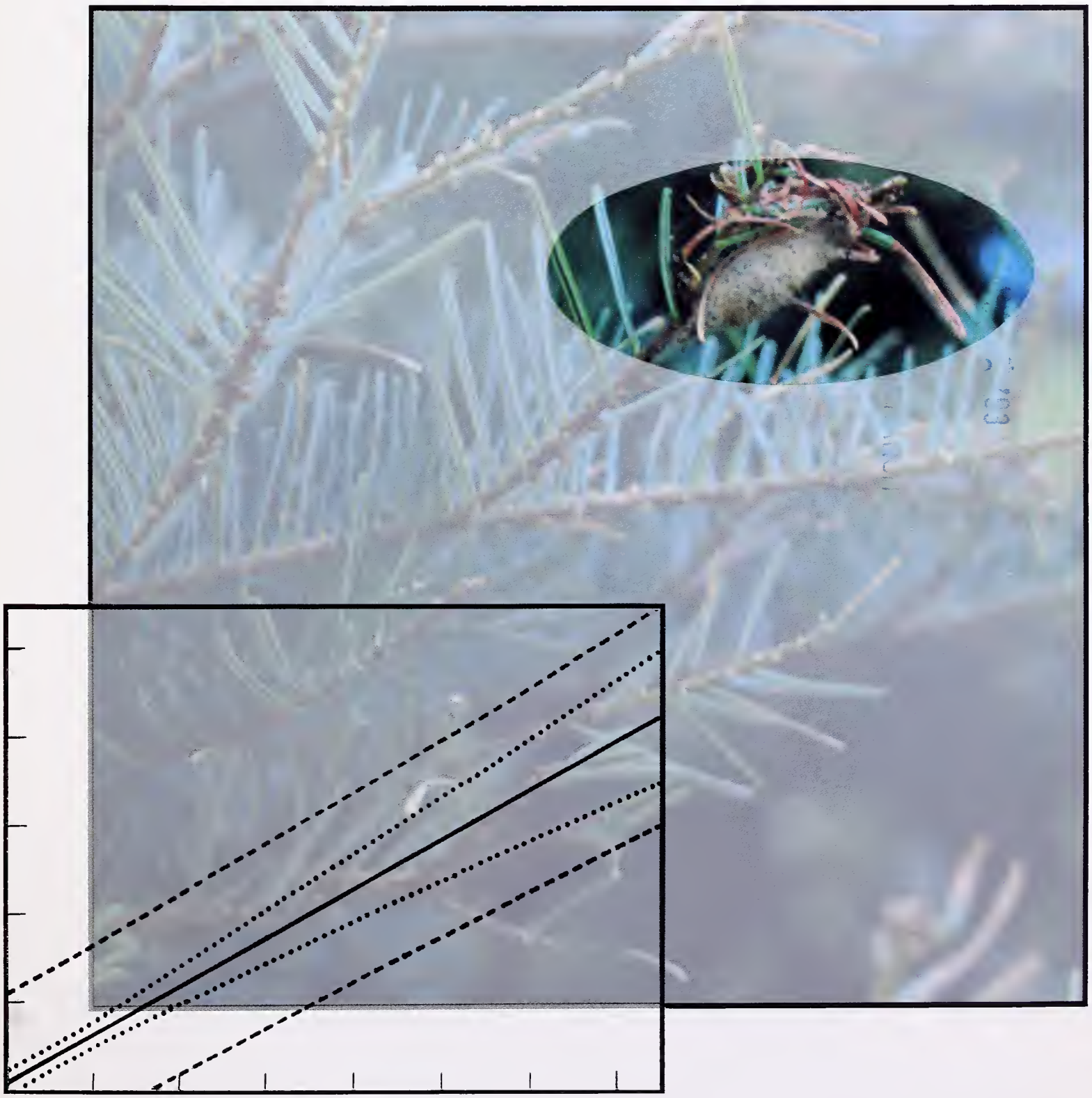
Forecasting Outbreaks of the Douglas-Fir Tussock Moth From Lower Crown Cocoon Samples

R.R. Mason, D.W. Scott, and H.G. Paul



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Abstract

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A predictive technique using a simple linear regression was developed to forecast the midcrown density of small tussock moth larvae from estimates of cocoon density in the previous generation. The regression estimator was derived from field samples of cocoons and larvae taken from a wide range of nonoutbreak tussock moth populations. The accuracy of the predictions was demonstrated on an operational basis in an independent tussock moth outbreak.

Keywords: Predicting insect populations, insect outbreaks, sampling insects, Douglas-fir tussock moth, *Orgyia pseudotsugata*.

Summary

The ability to predict outbreak populations in advance of damaging tree defoliation is critical to effective management of the Douglas-fir tussock moth (*Orgyia pseudotsugata* McDunnough). By comparing fall cocoon densities in nonoutbreak populations with larval densities the following spring, we showed that cocoon density is a good predictor of the next generation of larvae. The analysis was of six independent data sets collected over 14 years from populations in California, Oregon, and Washington. Two significantly different linear regressions were found to represent the range of observed relations between larval and cocoon densities. One regression forecasted sharply higher larval densities for the same cocoon density than the other regression. By pooling all data, a common regression estimator with 95-percent confidence limits was derived that represents most kinds of numerical behavior likely to be encountered in rising tussock moth populations. On average, increasing populations are predicted to have 55 to 65 more larvae in the spring for each pupa sampled in the previous fall. Recommendations are given for sampling cocoons on lower tree branches and for the number of plots needed for a desired precision of estimate. The technique is proposed for use in stands recently having an increase in tussock moth activity but not yet showing visible tree defoliation. The overall accuracy and potential usefulness of the predictive method was confirmed by operational sample data in an independent tussock moth outbreak.

Introduction

Predicting population trends is a critical part of the biological evaluation process in the management of important forest insect pests. Various sampling schemes and analyses have been proposed for predicting larval densities of the Douglas-fir tussock moth (*Orgyia pseudotsugata* McDunnough)(Mason 1969, Mason and Overton 1983, Mason and Torgersen 1987). Many of these techniques, unfortunately, require previous population data that are either unavailable or impractical to collect on a large scale. Tussock moth outbreaks always are preceded by several years of consecutive population increases that are easily detected by conventional methods of monitoring adults or larvae (Daterman and others 1979, Mason 1979, Shepherd and others 1985). Once the buildup reaches suboutbreak density (that is, relatively large number of insects not yet causing noticeable defoliation), an outbreak with tree damage can follow in the next generation. All populations reaching suboutbreak densities do not necessarily continue on to become outbreaks but often return to a low density without causing significant defoliation. Reliable and efficient techniques are needed to predict whether or not a given suboutbreak population is likely to develop into a damaging outbreak.

Numbers of fall egg masses customarily have been used to predict spring larval densities in potential outbreak situations (Mason 1969, Shepherd and others 1985). Egg masses that are laid on the surface of female cocoons, however, are difficult to sample in suboutbreak populations because they are still relatively rare and often concentrated in the upper crowns of trees (Mason 1970, Sower and others 1983). Cocoons of both sexes also may be scarce, but they are at least twice as common as egg masses on lower crown branches where they are easily detected (Luck and Dahlsten 1980). Although pupae in cocoons are two life stages removed from the next larval generation, they may be nearly as good an indicator of subsequent larval numbers as eggs and are much easier to sample. For these reasons, we chose to evaluate fall cocoon density on branches in the lower crown as a possible predictor of midcrown larval density in the next year.

To develop a general relation between the density of cocoons and larvae that would have wide application, data had to be collected from a range of rising populations not yet at outbreak numbers. After an outbreak occurs, the relation between cocoon and larval densities is less reliable because of greater variability contributed by the increasing mortality of pupae and eggs. Tussock moth cocoons are rare or locally extinct in stands most of the time, so considerable serendipity was involved in finding populations where cocoons could be sampled but had not yet caused defoliation of trees. In this paper, we show the relation between cocoons and small larvae in data sets collected from a wide range of nonoutbreak tussock moth populations.

Methods

Location and Description of Sample Areas

Data were collected from tussock moth populations in the Eldorado National Forest in northern California, the Okanogan and Wenatchee National Forests in north-central Washington, and the Umatilla and Wallowa-Whitman National Forests in northeastern Oregon. Typical forest composition at sample sites was a mixed-conifer type of ponderosa pine (*Pinus ponderosa* Dougl. ex Laws), true fir (*Abies* spp.), and Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco.). In California, sample sites were dominated by tussock moth host species of white fir (*Abies concolor* (Gord.and Glend.) Lindl. ex. Hildebr.) and Douglas-fir; in Washington, Douglas-fir was the prevailing host tree; and in Oregon, grand fir, (*Abies grandis* (Dougl. ex D. Don) Lindl.) in association with Douglas-fir was dominant. Most sample sites had a history of outbreaks of the Douglas-fir tussock moth or had been monitored annually for tussock moth activity as part of other research studies.

Estimation of Pupal and Larval Densities

A sample plot was 50 randomly selected host trees having lower branches within reach from the ground with the trees distributed over 2 to 5 acres (0.8 to 2.0 ha). Plots were selected for the study and sampled for cocoons only if they were expected to have measurable larval populations the next summer. Cocoons were sampled in the fall after moth emergence and oviposition. First and second instars were sampled on the same plots the following June. Densities were estimated in each plot by the frequency of occurrence of tussock moth (that is, cocoons in the fall or larvae in the summer) on the lower branches of 50 host trees (Mason 1977, 1979, 1987). With this method for sampling cocoons, the underside of three 18-inch (45-cm) branch tips in the lower crown was visually examined on each tree for the presence or absence of cocoons. The proportion, p, of infested sample trees on the plot was then converted to density of cocoons/1000 square inches (0.65 m^2) of branch area, X, by the theoretical distribution of the Poisson series (Mason 1977) where,

$$X = -2 \ln(1-p) . \qquad (1)$$

The same procedure was repeated for sampling small larvae in the summer, except that branches in the same stratum were beaten over a handheld dropcloth (Paul 1979) to observe the presence or absence of larvae. In a few cases where outbreak populations of larvae had developed and all trees were infested, the number of larvae on the samples had to be counted and related to the total branch area sampled. Whereas cocoons were expressed in terms of lower crown density, larvae were converted to their conventional expression of midcrown density by increasing the lower crown estimate by a factor of 2.0 (Mason 1977).

Analysis

The paired estimates of lower crown cocoon density and midcrown larval density were sorted into data sets by geographic location and year. Each data set was analyzed by simple linear regression in which the dependent variable, summer larval density, was regressed on the independent variable, fall cocoon density of the previous year. Differences in intercepts and slopes of the regressions were tested by analysis of covariance. Common linear regressions were calculated for data sets that were not statistically different at the 0.05 probability level and for all paired estimates combined.

Results and Discussion

Data Sets

Six data sets of paired cocoon vs. larval densities (cocoons in one generation and larvae in the next) were collected over 14 years (table 1). The data in each set came from tussock moth populations in the same National Forest and usually from the same two consecutive generations. The only exception was a data set from the Wallowa-Whitman National Forest that included cocoon and larval densities estimated for consecutive generations in 1982-83 as well as in 1983-84. The number of paired observations in a set ranged from 6 to 15. Many other plots were sampled in the same time span but were not included among the analyzed data because the estimates of density were zero for both cocoons and larvae.

Table 1—Data sets of paired estimates of cocoon and larval densities of the Douglas-fir tussock moth in 2 consecutive generations at 6 locations

National Forest	Geographic location	Years of samples (cocoons/larvae)	Sampled density: Cocoons (lower crown)	Sampled density: Larvae (midcrown)
			- - No./1000 square inches - -	
Eldorado	Northern California	1978/1979	0.17	7.94
			.30	10.18
			.45	12.95
			.50	12.95
			0	.97
			.04	2.85
			.26	8.56
			.26	5.47
Okanogan/Wenatchee	Central Washington	1981/1982	.02	.25
			.08	2.77
			.02	1.43
			0	.16
			0	1.72
			.02	1.15
Wallowa-Whitman	Northeast Oregon	1982/1883	.02	3.28
			.17	1.78
		1983/1984	0	.85
			0	.08
			0	.16
			0	.08
Wallowa-Whitman	Northeast Oregon	1989/1990	.08	11.79
			0	9.09
			.08	13.82
			.04	9.20
			0	12.88
			0	28.40
			.66	64.72
			1.16	76.64
			.89	75.52
			.21	16.96
			.50	21.36
			.08	6.56
			.26	42.64
			.17	12.00
			0	14.00
Umatilla	Northeast Oregon	1989/1990	0	.09
			0	.27
			.04	0
			0	0
			0	1.75
			.12	2.61
			0	1.68
			.04	3.40
			.04	1.82
			0	.09

Continued next page.

Table 1—Data sets of paired estimates of cocoon and larval densities of the Douglas-fir tussock moth in 2 consecutive generations at 6 locations (continued)

National Forest	Geographic location	Years of samples (cocoons/larvae)	Sampled density: Cocoons (lower crown)	Sampled density: Larvae (midcrown)
			- - No./1000 square inches - -	
Umatilla	Northeast Oregon	1990/1991	0	.18
			.04	.09
			.08	.18
			.08	0
			.17	12.56
			.89	21.11
			.04	13.03
			.40	17.17
			.17	7.97
			0	.27
			.30	9.39
			0	.06

Comparison of Regression Lines

The calculated regressions of larval density on cocoon density produced positive intercepts and slopes for each data set, although the coefficients were variable and not always statistically significant at $p = 0.05$ (table 2, part A). The regression lines for five of the data sets were bunched or overlapped, while the line of the sixth set (WW 1989-90) was separated from the other lines by a higher intercept and steeper slope (fig. 1). When all six regression lines were compared together in a separate covariance analysis, both the slopes and intercepts among the lines were significantly different ($p < 0.01$). When the odd line (D in fig. 1) was removed and the same test performed again, the slopes and intercepts of the remaining five lines no longer differed ($p = 0.93$ and 0.52, respectively). This indicated that the odd line is significantly different from the others, whereas the five similar lines are most likely coincident and could be represented by the same regression.

The above results suggest that the data sets included two general types of predictive behavior, with one forecasting sharply higher larval densities for the same pupal density than the other. These behavior types are illustrated by the two significantly different regression lines in figure 2. The divergent slopes of the lines probably are caused by different survival or reproductive rates, or both, in the inclusive populations between the pupal and early larval life stages. The steeper line (I in fig. 2) apparently reflects a "releasing" population initiating the peak phase of a tussock moth outbreak, whereas the flatter line (II in fig. 2) is charactersitic of populations more constrained by natural regulation (Mason and Wickman 1988).

Table 2—Regression statistics for separate and combined data sets

Data set	Regression coefficients: Intercept	Regression coefficients: Slope	r^2	F-value for slope	Error degrees of freedom	Pr>F
A. Separate:[a]						
a - EL 1978-79	1.88	23.63	0.897	52.12	6	<0.01
b - OW 1981-82	.69	23.92	.521	4.35	4	.11
c - WW 1982-83, 1983-84	.81	7.34	.153	.72	4	.44
d - WW 1989-90	10.61	62.09	.822	59.98	13	<.01
e - UM 1989-90	.74	17.93	.310	3.59	8	.09
f - UM 1990-91	2.42	24.43	.655	18.96	10	<.01
B. Combined:						
Data sets a,b,c,e,f	1.11	26.01	.756	123.96	40	<.01
All data	1.70	55.14	.660	106.94	55	<.01

[a] EL = Eldorado National Forest, OW = Okanogan and Wenatchee, WW = Wallowa-Whitman, and UM = Umatilla.

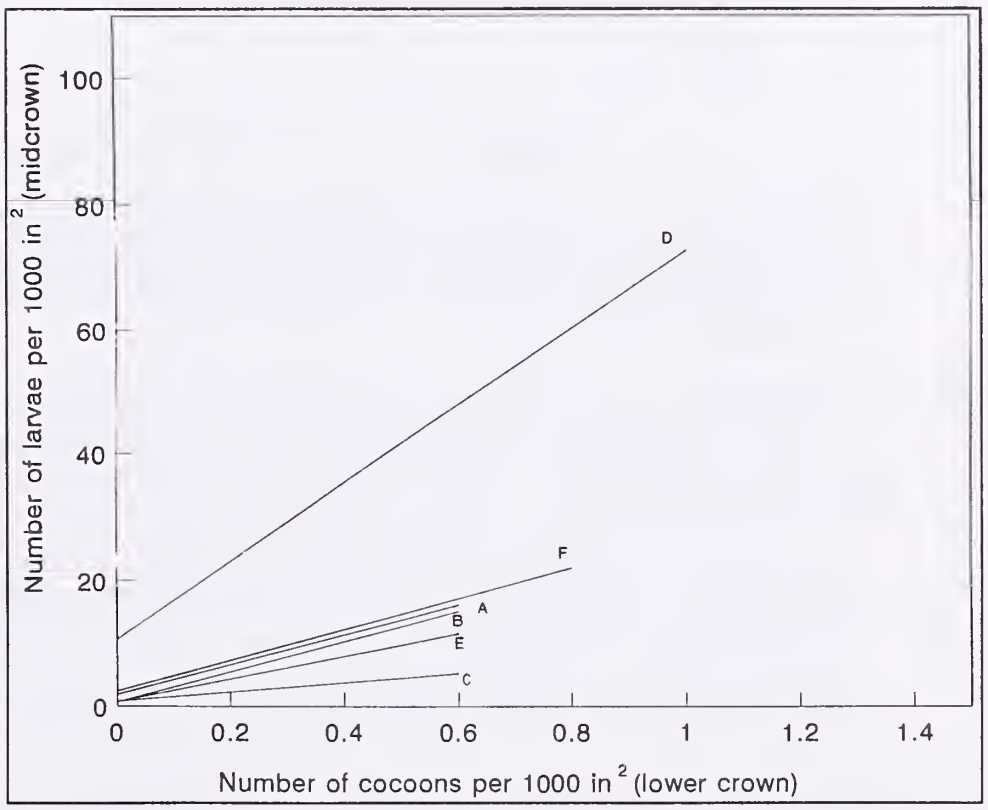

Figure 1—Regression lines of larval density on cocoon density for individual data sets: A—Eldorado 1978-79; B—Okanogan and Wenatchee 1981-82; C—Wallowa-Whitman 1982-83 and 1983-84; D—Wallowa-Whitman 1989-90; E—Umatilla 1989-90; and F—Umatilla 1990-91.

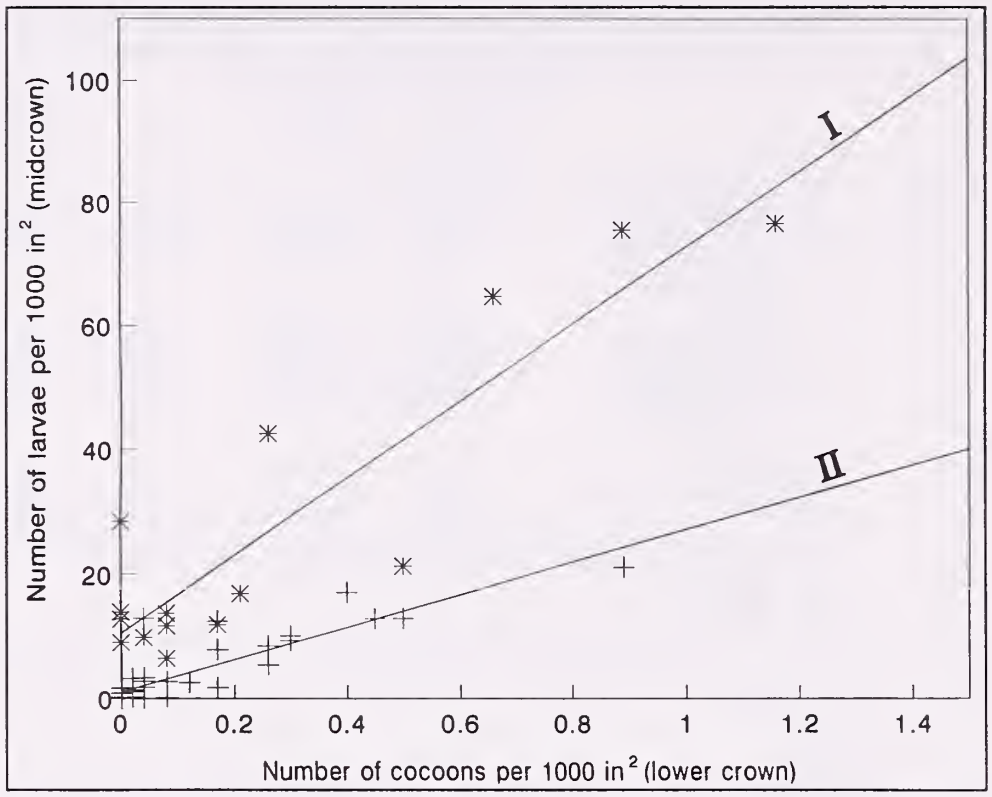

Figure 2—Regression lines of larval density on cocoon density and associated data points for two significantly different types of numerical behavior. I (•) = data set: Wallowa-Whitman 1989-90. II (+) = combined data sets: Eldorado 1978-79, Okanogan and Wenatchee 1981-82, Wallowa-Whitman 1982-83, 1983-84, Umatilla 1989-90, and Umatilla 1990-91.

Common Regression Estimator

Although the available data suggest more than one type of numerical behavior, they should be pooled for predictive purposes in a common regression to represent all kinds of behavior that might be encountered. At our current state of knowledge, we are not likely to know a priori how a given population is going to behave numerically; therefore, the regression estimator should reflect a variety of conditions and the uncertainty inherent in each prediction. The best predictive model for estimating larval density in all situations is the linear regression equation calculated from the combined set of all paired observations (table 2, part B),

$$Y = 1.70 + 55.14\ X\ , \qquad (2)$$

where Y is the number of small larvae/1000 square inches in the midcrown and X is the number of cocoons/1000 square inches in the lower crown the previous fall (fig. 3). Because the data base is strongly weighted by the set of observations (WW 1989-90, table 2, part A) in which predicted larval densities are especially high relative to other data sets, it can be expected that the regression may overestimate more populations than it underestimates. The confidence bands in figure 3 give the probable limits of larval density when estimated from the mean of a series of plots ($\hat{\bar{Y}}$) and when estimated from an individual plot ($\hat{Y}$) for any given value of X.

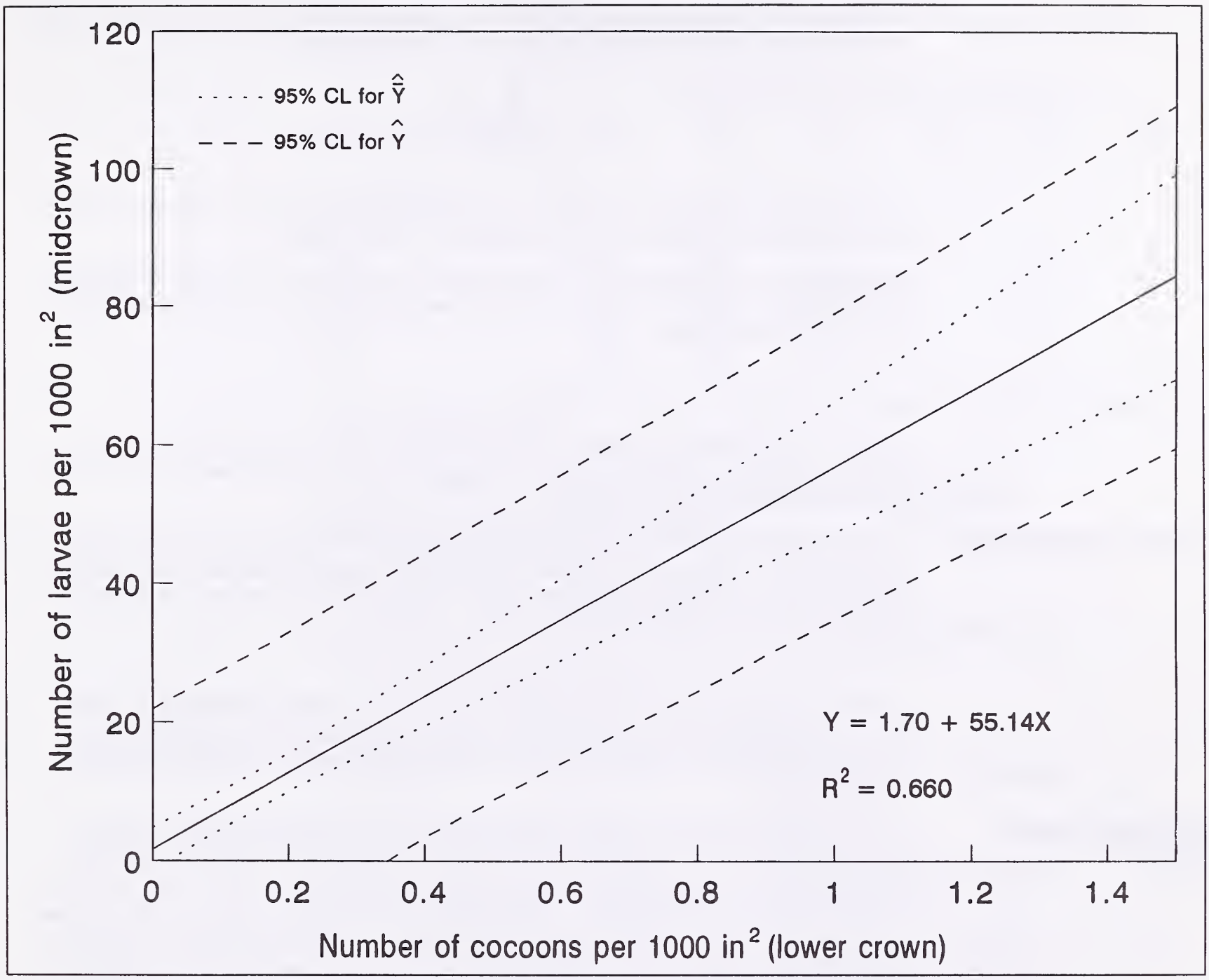

Figure 3—Common regression line of larval density on cocoon density for all data points with 95-percent confidence limits for mean ($\hat{\bar{Y}}$) and individual ($\hat{Y}$) predictions.

Application

Estimation of Cocoon Density

Before the forecasting technique using equation (2) can be applied, the density of cocoons in fall must be determined in the area for which the forecast is to be made. We recommend doing this for a series of plots by sampling the lower branches of 20 to 50 host trees per plot. The primary sampling unit on each tree is three 18-inch branch tips randomly selected in the lower crown. Each three-branch sample unit contains about 500 square inches (0.32 m^2) (Mason 1977). Pupal density on a plot can be estimated either by a total count of all cocoons on the three-branch sample units or by determining the frequency of occurrence of cocoons on the sample units.

Total count—All cocoons on the three-branch sample units are counted and related to the total branch area observed by,

$$X = \frac{2\sum_{i=1}^{n} y_i}{n}, \qquad (3)$$

where X is the number of cocoons/1000 square inches, y_i is the number of cocoons on the i'th sample unit, and n is the number of sample trees.

Frequency of occurrence—Each three-branch sample unit is visually examined for the presence or absence of cocoons and the proportion, *p*, of all sample units that are infested is calculated by,

$$p = \frac{r}{n}, \qquad (4)$$

where r is the number of sample units with one or more cocoons and n is the number of trees sampled. Cocoon density for the plot is determined by substituting *p* in equation (1) and solving for X.

Number of Sample Plots

The number of plots to sample depends on the expected variance between plots and the precision wanted in the cocoon sample. When interplot variance was calculated for five of the six original data sets given in table 1, it was found to vary significantly with the mean according to the power law,

$$s^2 = 0.46\, m^{1.65}, \qquad (5)$$

where s^2 is the variance between plots and m is the mean of plots (Taylor 1961). The number of plots needed for a desired precision, therefore, is estimated for any expected mean cocoon density by solving the standard sample-size equation (table 3).

Forecasting Larval Density

After estimating cocoon density, larval density can be predicted easily either by solving equation (2) or by reading the curve in figure 3. The regression estimator shows that, on average, preoutbreak populations are likely to have 55 to 65 times more larvae in the spring than cocoons in the previous fall. Because of the relatively wide confidence bands for individual plot estimates, forecasts should be based on an estimated mean of several plots (table 3). Ultimately, the predictive model may be most useful in defining critical thresholds rather than in giving predictions over a continuous range of values. For example, if a density of 20 small larvae/1000 square inches is taken to be the threshold for visible tree defoliation, then a mean density of fewer than 0.3 cocoons/1000 square inches on lower branches in the fall is not likely to result in an outbreak the next summer (table 4). By the same token, a mean cocoon density larger than 0.7/1000 square inches almost surely will forecast significant tree defoliation.

Table 3—Number of plots required to estimate cocoon densities at different levels of precision when sampling 50 trees per plot[a]

	Standard error as percent of the mean					
Mean cocoon density	10	20	30	40	50	60
No./1000 in²						
0.20	81	20	9	5	3	2
0.40	64	16	7	4	3	2
0.60	55	14	6	3	2	2
0.80	50	12	6	3	2	1
1.00	46	11	5	3	2	1
1.20	43	11	5	3	2	1
1.40	41	10	5	3	2	1

[a] Sample size, n, was calculated by solving the equation $n = s_2/s^2_{\bar{x}}$ where s^2 is between-plot variance and $s_{\bar{x}}$ the desired standard error.

Table 4—Relation of estimated cocoon densities in preoutbreak populations of the Douglas-fir tussock moth to predicted larval densities and status in the next generation

Range of cocoon densities in the lower crown	Predicted larval densities in the midcrown	Predicted population status
– – – – No./1000 square inches – – – –		
<0.01	<2.0	Low density; no defoliation
0.01-0.30	2.0-20.0	Suboutbreak; little or no visible defoliation
0.31-0.70	21.0-40.0	Moderate outbreak; defoliation visible on most host trees
>0.70	>40.0	Severe outbreak; defoliation intense in upper crowns of many host trees with some trees completely defoliated

Validation

An early version of the prediction equation was tested operationally in an incipient outbreak of the Douglas-fir tussock moth on the Wallowa-Whitman National Forest in fall 1990. More than 500 plots of 20 trees each were sampled for cocoons to determine the extent of the outbreak and to identify larval populations that might need control the next summer.[1] To confirm the accuracy of forecasts made from the fall cocoon survey, selected portions of the infested area were resampled for tussock moth larvae in summer 1991.

Certain problems were encountered in the operational sampling that made precise comparisons of predicted and observed results difficult. For example, cocoon sample points were located by legal description of township, range, and section, with the section the smallest unit recorded. As a result, comparisons of predicted vs. observed larval densities had to be made for a broader geographical area than if estimates had been made for the same plots of 20 identical trees. The composition of larval instars sampled in 1991 also were frequently older than the first and second instars assumed in the prediction model. This necessitated the backdating of sampled estimates to the probable density of these early instars by using estimates of larval survival for the same stages calculated from nearby areas.[2]

Despite the difficulties of reproducing data from identical areas, comparisons of results from plots in the same vicinity were made with some success. Data pairs consisting of "predicted" and "observed" values from 35 similar geographical areas were compared (fig. 4). The data points are widely scattered around the 1-to-1 slope where Y = X, but this is not surprising for individual plots, which are expected to have considerable variability (fig. 3). The "observed" means of several plots undoubtedly would more nearly approach the "predicted" means for the same plots. The close relation of the fitted regression of all data pairs to the 1-to-1 line in figure 4 demonstrates the overall accuracy of the prediction equation when applied to an independent population and confirms its potential usefulness in a practical situation.

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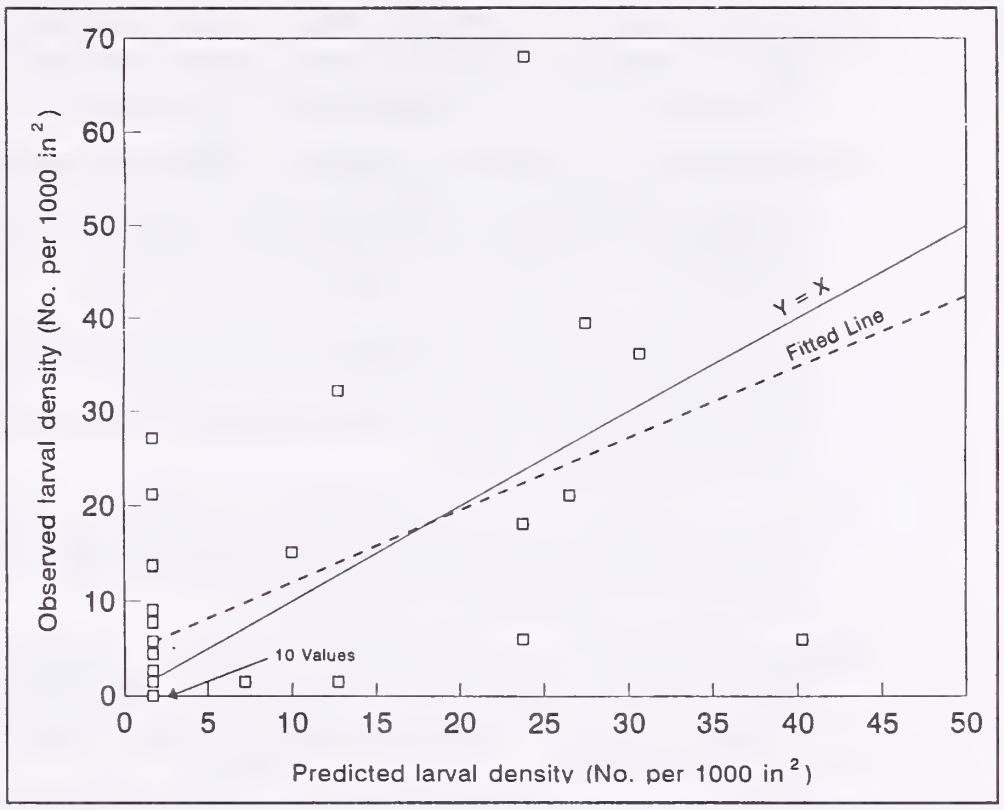

Figure 4—Comparison of midcrown larval densities predicted by sampling cocoons with those observed by direct sampling of larvae on plots in the same township, range, and section. The solid line is the expected relation between observed and predicted densities. The dashed line is the linear best fit by least squares (r^2 = 0.304; $p < 0.01$; $n = 35$) of the actual relation between observed and predicted densities.

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Penalty for Private Use, $300

do NOT detach label